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RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/10/051,909

TIME: 12:40:00

Input Set : A:\BB1163 US CIP Seq Listing.txt

Output Set: N:\CRF3\02072002\J051909.raw

2 <110> APPLICANT: Allen, Steve
3 Helentjaris, Tim
4 Hitz, Bill
5 Kinney, Tony
6 Tingey, Scott
8 <120> TITLE OF INVENTION: Plant Sugar Transport Proteins
10 <130> FILE REFERENCE: BB1163 US CIP
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/051,909
C--> 13 <141> CURRENT FILING DATE: 2002-01-17
15 <150> PRIOR APPLICATION NUMBER: 60/083,044
W--> 16 <151> PRIOR FILING DATE: April 24, 1998
18 <160> NUMBER OF SEQ ID NOS: 38
20 <170> SOFTWARE: Microsoft Office 97
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2824
24 <212> TYPE: DNA
25 <213> ORGANISM: Zea mays
27 <220> FEATURE:
28 <221> NAME/KEY: unsure
29 <222> LOCATION: (29)
31 <220> FEATURE:
32 <221> NAME/KEY: unsure
33 <222> LOCATION: (622)
35 <220> FEATURE:
36 <221> NAME/KEY: unsure
37 <222> LOCATION: (636)
39 <220> FEATURE:
40 <221> NAME/KEY: unsure
41 <222> LOCATION: (638)
43 <220> FEATURE:
44 <221> NAME/KEY: unsure
45 <222> LOCATION: (669)
47 <220> FEATURE:
48 <221> NAME/KEY: unsure
49 <222> LOCATION: (771)
51 <220> FEATURE:
52 <221> NAME/KEY: unsure
53 <222> LOCATION: (822)
55 <220> FEATURE:
56 <221> NAME/KEY: unsure
57 <222> LOCATION: (856)
59 <220> FEATURE:
60 <221> NAME/KEY: unsure

ENTERED

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61 <222> LOCATION: (889)
63 <220> FEATURE:
64 <221> NAME/KEY: unsure
65 <222> LOCATION: (896)
67 <220> FEATURE:
68 <221> NAME/KEY: unsure
69 <222> LOCATION: (944)
71 <400> SEQUENCE: 1

W--> 72 cccaccccc tccactccac taccacggng gcacggcctg cctctgcagc tctgccctgc 60
73 tccgcacccc tcgctctcca accccaacgc gcggcgttgc taaaattcac ctcagcgcgt 120
74 actccagttt ggccacctca ccacccgcgc ccgctgttta agaaggcccc gcgcccgatc 180
75 ggggatcacg aaccttggcc gccgctgccg gagtgggggc gtagatttcc ggcggccatg 240
76 gggggcgcgc tgatggtcgc catcgccgcc tctatcgcca acttgctgca gggctgggac 300
77 aatgcgacaa ttgctggagc cgctcgttac ataaagaagg aattcaacct gcagagcgag 360
78 cctctgatcg aaggccctcat cgtcgccatg ttcctcattg gggcaacagt catcacaaca 420
79 tctccggggc caagggttga ctgcgtttgt aggaggccca tgctggctgc ctcggctgtc 480
80 ctctacttgc tcagtgggct ggtgatgctt tgggcgccaa ttgtgtacat cttgcctctc 540
81 gcaaggctca ttgatgggtt cggtatcggt ttggcgggtc cacttgttcc tctctacatc 600
W--> 82 tccgaaactg caccgcacag ahattcttgg ggctgntnga acacgttgcc gcagttcatt 660
W--> 83 ggggtcagn gagggatgtt cctctctac tgcatggtgt ttgggatgtc cctcatgccc 720
W--> 84 aaacctgatt ggaggtcat gcttggagtt ctgtcgatcc cgctcattat ntactttgga 780
W--> 85 ctgactgtct tctacttgc tgaatcacca aggtggcttg tnagcaaagg aaggatggcg 840
W--> 86 gaggcgaaga gagtgnatga aaggctgcgg ggaagagaag atgtctcang ggaganggct 900
W--> 87 cttctagtgt aaggtttggg ggtcggtaaa gatacacgta tttnagagta catcattgga 960
88 cctgccaccg aggcagccga tgatcttcta actgacggtg ataaggaaca aatcacactt 1020
89 tatgggcctg aagaaggcca gtcatggatt gctcgacctt ctaagggacc catcatgctt 1080
90 ggaagtgtgc tttctcttgc atctcgtcat gggagcatgg tgaaccagag tgtacccttt 1140
91 atggatccga ttgtgacact ttttggtagt gtccatgaga atatgcctca agctggagga 1200
92 agtatgagga gcacattgtt tccaaacttt ggaagtatgt tcagtgtcac agatcagcat 1260
93 gccaaaaatg agcagtggga tgaagagaat cttcataggg atgacgagga gtacgcattc 1320
94 gatggtgcag gaggtgacta tgaggacaat ctccatagcc cattgctgtc caggcaggca 1380
95 acaggtgcgg aaggggaagg cattgtgcac catggtcacc gtggaagtgc tttgagcatg 1440
96 agaaggcaaa gcctcttagg ggaggggtga gatggtgtga gcagcactga tatcgggtgg 1500
97 ggatggcagc ttgcttggaa atggtcagag aagggaagtg agaatggtag aaaggaaggt 1560
98 ggtttcaaaa gagtctactt gcaccaagag ggagttcctg gctcaagaag gggctcaatt 1620
99 gtttcaactt ccggtggtgg cgatgttctt gagggtagtg agtttgtaca tgctgctgct 1680
100 ttagtaagtc agtcagcact tttctcaaa ggtcttgctg aaccacgcac gtcagatgct 1740
101 gccatggttc acccatctga ggtagctgcc aaaggttcac gttggaagaa tttgtttgaa 1800
102 cctggagtga ggcgtgccct gttagtcggt gttggaattc agatccttca acagtttgct 1860
103 ggaataaacg gtgttctgta ctatacccca caaattcttg agcaagctgg tgtggcagtt 1920
104 attctttcca aatttggctt cagctcgcca tcagcatcca tottgatcag ttctctcact 1980
105 accttactaa tgttctcttg cattggcttt gccatgctgc ttatggatct ttccggaaga 2040
106 aggtttttgc tgctaggcac aattccaatc ttgatagcat ctctagttat cctggttggt 2100
107 tccaatctaa ttgatttggg tacactagcc catgctttgc tctccaccat cagtgttatc 2160
108 gtctacttct gctgcttcgt tatgggattt ggtcccatcc ccaacatttt atgtgcagag 2220
109 atctttccaa ccagggttcg tggcctctgt attgccattt gtgcctttac attctggatc 2280
110 ggagatatca tcgtcaccta cagccttctt gtgatgctga atgctatttg actggcgggt 2340
111 gttttcagca tatatgcagt cgatgcttgc atttctcttg tgctcgtctt ccttaagggtc 2400
112 cctgagacaa aggggatgcc ccttgaggtt attaccgaat tctttgcagt tggtgcgaag 2460

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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113 caagcggctg caaaagccta atttctttgg tacctttgtg tgcaactatt gcactgtgaag 2520
114 ttagaaactt gaaggggttt caccaagaag ctcgagagaat tactttggat ttgtgtaaat 2580
115 gttaaggga cgaacatctg ctcatgctcc tcaaacggta aaaaagagtc cctcaatggc 2640
116 aaataggagt cgtaaagttg tcaatgtcat ttaccatag ttttacctat ttgtactgta 2700
117 ttataagtca agctattcaa cgctggttgt tgctagaaat ctttagaaca aagatgataa 2760
118 tgatctgatc tgatgttata atattcaaat ctcaaataaa gaaaatatcg tttctcaaaa 2820
119 aaaa 2824
121 <210> SEQ ID NO: 2
122 <211> LENGTH: 747
123 <212> TYPE: PRT
124 <213> ORGANISM: Zea mays
126 <220> FEATURE:
127 <221> NAME/KEY: UNSURE
128 <222> LOCATION: (129)
130 <220> FEATURE:
131 <221> NAME/KEY: UNSURE
132 <222> LOCATION: (133)..(134)
134 <220> FEATURE:
135 <221> NAME/KEY: UNSURE
136 <222> LOCATION: (144)
138 <220> FEATURE:
139 <221> NAME/KEY: UNSURE
140 <222> LOCATION: (178)
142 <220> FEATURE:
143 <221> NAME/KEY: UNSURE
144 <222> LOCATION: (207)
146 <220> FEATURE:
147 <221> NAME/KEY: UNSURE
148 <222> LOCATION: (218)
150 <220> FEATURE:
151 <221> NAME/KEY: UNSURE
152 <222> LOCATION: (220)
154 <220> FEATURE:
155 <221> NAME/KEY: UNSURE
156 <222> LOCATION: (236)
158 <400> SEQUENCE: 2
159 Met Gly Gly Ala Val Met Val Ala Ile Ala Ala Ser Ile Gly Asn Leu
160 1 5 10 15
162 Leu Gln Gly Trp Asp Asn Ala Thr Ile Ala Gly Ala Val Leu Tyr Ile
163 20 25 30
165 Lys Lys Glu Phe Asn Leu Gln Ser Glu Pro Leu Ile Glu Gly Leu Ile
166 35 40 45
168 Val Ala Met Phe Leu Ile Gly Ala Thr Val Ile Thr Ser Pro Gly
169 50 55 60
171 Pro Arg Ala Asp Cys Val Gly Arg Arg Pro Met Leu Val Ala Ser Ala
172 65 70 75 80
174 Val Leu Tyr Phe Val Ser Gly Leu Val Met Leu Trp Ala Pro Ile Val
175 85 90 95
177 Tyr Ile Leu Leu Leu Ala Arg Leu Ile Asp Gly Phe Gly Ile Gly Leu

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```

178          100          105          110
180 Ala Val Thr Leu Val Pro Leu Tyr Ile Ser Glu Thr Ala Pro His Arg
181          115          120          125
W--> 183 Xaa Ser Trp Gly Xaa Xaa Asn Thr Leu Pro Gln Phe Ile Gly Val Xaa
184          130          135          140
186 Gly Gly Met Phe Leu Ser Tyr Cys Met Val Phe Gly Met Ser Leu Met
187 145          150          155          160
189 Pro Lys Pro Asp Trp Arg Leu Met Leu Gly Val Leu Ser Ile Pro Ser
190          165          170          175
W--> 192 Leu Xaa Tyr Phe Gly Leu Thr Val Phe Tyr Leu Pro Glu Ser Pro Arg
193          180          185          190
W--> 195 Trp Leu Val Ser Lys Gly Arg Met Ala Glu Ala Lys Arg Val Xaa Gln
196          195          200          205
W--> 198 Arg Leu Arg Gly Arg Glu Asp Val Ser Xaa Glu Xaa Ala Leu Leu Val
199          210          215          220
W--> 201 Glu Gly Leu Gly Val Gly Lys Asp Thr Arg Ile Xaa Glu Tyr Ile Ile
202 225          230          235          240
204 Gly Pro Ala Thr Glu Ala Ala Asp Asp Leu Val Thr Asp Gly Asp Lys
205          245          250          255
207 Glu Gln Ile Thr Leu Tyr Gly Pro Glu Glu Gly Gln Ser Trp Ile Ala
208          260          265          270
210 Arg Pro Ser Lys Gly Pro Ile Met Leu Gly Ser Val Leu Ser Leu Ala
211          275          280          285
213 Ser Arg His Gly Ser Met Val Asn Gln Ser Val Pro Leu Met Asp Pro
214          290          295          300
216 Ile Val Thr Leu Phe Gly Ser Val His Glu Asn Met Pro Gln Ala Gly
217 305          310          315          320
219 Gly Ser Met Arg Ser Thr Leu Phe Pro Asn Phe Gly Ser Met Phe Ser
220          325          330          335
222 Val Thr Asp Gln His Ala Lys Asn Glu Gln Trp Asp Glu Glu Asn Leu
223          340          345          350
225 His Arg Asp Asp Glu Glu Tyr Ala Ser Asp Gly Ala Gly Gly Asp Tyr
226          355          360          365
228 Glu Asp Asn Leu His Ser Pro Leu Leu Ser Arg Gln Ala Thr Gly Ala
229          370          375          380
231 Glu Gly Lys Asp Ile Val His His Gly His Arg Gly Ser Ala Leu Ser
232 385          390          395          400
234 Met Arg Arg Gln Ser Leu Leu Gly Glu Gly Gly Asp Gly Val Ser Ser
235          405          410          415
237 Thr Asp Ile Gly Gly Gly Trp Gln Leu Ala Trp Lys Trp Ser Glu Lys
238          420          425          430
240 Glu Gly Glu Asn Gly Arg Lys Glu Gly Gly Phe Lys Arg Val Tyr Leu
241          435          440          445
243 His Gln Glu Gly Val Pro Gly Ser Arg Arg Gly Ser Ile Val Ser Leu
244          450          455          460
246 Pro Gly Gly Gly Asp Val Leu Glu Gly Ser Glu Phe Val His Ala Ala
247 465          470          475          480
249 Ala Leu Val Ser Gln Ser Ala Leu Phe Ser Lys Gly Leu Ala Glu Pro
250          485          490          495

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```

252 Arg Met Ser Asp Ala Ala Met Val His Pro Ser Glu Val Ala Ala Lys
253                               500                               505                               510
255 Gly Ser Arg Trp Lys Asp Leu Phe Glu Pro Gly Val Arg Arg Ala Leu
256                               515                               520                               525
258 Leu Val Gly Val Gly Ile Gln Ile Leu Gln Gln Phe Ala Gly Ile Asn
259                               530                               535                               540
261 Gly Val Leu Tyr Tyr Thr Pro Gln Ile Leu Glu Gln Ala Gly Val Ala
262 545                               550                               555                               560
264 Val Ile Leu Ser Lys Phe Gly Leu Ser Ser Ala Ser Ala Ser Ile Leu
265                               565                               570                               575
267 Ile Ser Ser Ser Leu Thr Thr Leu Leu Met Leu Pro Cys Ile Gly Phe Ala
268                               580                               585                               590
270 Met Leu Leu Met Asp Leu Ser Gly Arg Arg Phe Leu Leu Leu Gly Thr
271                               595                               600                               605
273 Ile Pro Ile Leu Ile Ala Ser Leu Val Ile Leu Val Val Ser Asn Leu
274                               610                               615                               620
276 Ile Asp Leu Gly Thr Leu Ala His Ala Leu Leu Ser Thr Ile Ser Val
277 625                               630                               635                               640
279 Ile Val Tyr Phe Cys Cys Phe Val Met Gly Phe Gly Pro Ile Pro Asn
280                               645                               650                               655
282 Ile Leu Cys Ala Glu Ile Phe Pro Thr Arg Val Arg Gly Leu Cys Ile
283                               660                               665                               670
285 Ala Ile Cys Ala Phe Thr Phe Trp Ile Gly Asp Ile Ile Val Thr Tyr
286                               675                               680                               685
288 Ser Leu Pro Val Met Leu Asn Ala Ile Gly Leu Ala Gly Val Phe Ser
289                               690                               695                               700
291 Ile Tyr Ala Val Val Cys Leu Ile Ser Phe Val Phe Val Phe Leu Lys
292 705                               710                               715                               720
294 Val Pro Glu Thr Lys Gly Met Pro Leu Glu Val Ile Thr Glu Phe Phe
295                               725                               730                               735
297 Ala Val Gly Ala Lys Gln Ala Ala Ala Lys Ala
298                               740                               745
300 <210> SEQ ID NO: 3
301 <211> LENGTH: 443
302 <212> TYPE: DNA
303 <213> ORGANISM: Oryza sativa
305 <220> FEATURE:
306 <221> NAME/KEY: unsure
307 <222> LOCATION: (193)
309 <220> FEATURE:
310 <221> NAME/KEY: unsure
311 <222> LOCATION: (388)
313 <220> FEATURE:
314 <221> NAME/KEY: unsure
315 <222> LOCATION: (435)
317 <220> FEATURE:
318 <221> NAME/KEY: unsure
319 <222> LOCATION: (439)
321 <400> SEQUENCE: 3

```

Check for errors in the sequence listing. If errors are found, they should be corrected in the source file and the sequence listing should be regenerated. The sequence listing should be checked for errors using the following steps:

VERIFICATION SUMMARY

DATE: 02/07/2002

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:72 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:82 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:83 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:84 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:85 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:86 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:87 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:183 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:192 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:201 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:328 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:329 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:801 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:802 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1053 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1055 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1056 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1058 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17

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Input Set : A:\BB1163 US CIP Seq Listing.txt

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L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1060 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1061 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1095 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1104 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:1104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1116 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1335 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:1335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:2516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36